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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                   Database
                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein -
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                        seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using sw model
PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                      US-09-331-631A-5_COPY_145_210
375
                                                                                                                                                                                                                                                                                                                                                  1 KRDPQQREYEDCRRHCEQQE.....PQRGGSGRYEEGEEKQSDNP
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                                                                                                                                                                                                                                                               195891 seqs, 67900655 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
            pir1:*
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                                                                                                                                                                                                                                                                                                                                                                                                                   2001, 15:52:38; Search time 170.72 Seconds (without alignments) 26.250 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o	5	4	ω	2		No.	Result
71	71	71	71	71	71.5	71.5	72	72	73.5	74	74	74.5	75	75.5	76	76	77	78	78	79	81	84.5	84.5	95	116.5	120	121	129	Score	
18.9								19.2			19.7												•				•	34.4	Match	Query
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T18267	T08588	A39248	B54024	136911	A45973	T25169	A53234	S21825	JC5662	S27770	T01662	A34615	136912	A46419	A57783	T29475	I36930	A48686	T15132	S71628	D82493	T13998	T44430	S35221	S22477	S06398	FWCNAB	S08059	ID	
multidrug resistan	hypothetical prote	(†	se	•	_	۳		\mathbf{H}	Ξ.	10	ma		. involucrin S - dou	t-e			involucrin - white	probable RNA helic	ATP-dependent RNA	sensory transducti	conserved hypothet	stermin	n PV100 [im	_	rn -	tγ		alpha-globulin typ	Description	

ALIGNMENTS

A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. A;Reference number: A30838
A;Accession: A30838
A;Molecule type: mRNA
A;Residues: 1-588 <CHL>
A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C:Species: Gossyplum hirsutum (upland cotton) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C;Accession: A30838; 506911
R:Chlan C. A.: Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A; Molecule type: DNA A; Residues: 1-509 < CHL> C; Superfamily: glycinin alpha-globulin type B precursor (tandem 1) - upland cotton (fragment) R;Alternate names: seed storage protein C:Species: Gossypium hirsutum (upland cotton) C:Date: 31-Mar-1990 #sequence_revision.31-Mar-1990 #text_change 30-Sep-1993 C:Accession: S08059 B Qy В Qy A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. A;Reference number: S06398
A;Accession: S08059 A; Reference number: S06398 A; Title: Developmental_blochemistry of cottonseed embryogenesis and germination XVIII R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, Plant Mol. Biol. 9, 533-546, 1987 A; Status: not compared with conceptual translation Matches Query Match Best Local Similarity 60 KQQCVRECREKYQENPWRGEREEEAEEEETEEGEQEQSHNP 100 46 -----NPQRG-----GSGRYEEGEEKQSDNP 66 1 DPQRR-YEECQQECRQQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQOHCHQQEQRPEK 59 36; Conservative 34.4%; 9; Score 129; DB 2; Pred. No. 3.6e-06; Mismatches 18; r Length 509; Indels 38; PID: g167375 Gaps 5

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Plant Mol. Biol. 18, 1173-1176, 1992
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide sequence
A;Reference number: S22477; MUID:92288309
A;Accession: S22477
                                                                                                                                                                                                             C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                                   RESULT
S22477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: glycinin

F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Date: Jr. C. Accession: S06398
C:Accession: S06398
R:Chlan, C.A.: Borroto, K.: Kamalay, J.A.: Dure III,
R:Chlan, C.A.: 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein
                                                               A; Molecule type: DNA
A; Residues: 1-566 <MCH>
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
A; Molecule type: mRNA
                   A: Accession: S22478
                                           A; Cross-references: EMBL: X62625
                                                                                                                                                                                                                                                                               vicilin precursor - cacao
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A; Residues: 1-605 < CHL>
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A; Accession: S06398
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A;Title: Developmental biochemistry of cottonseed embryogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DPQQREYEDCRRHCEQQEPRL-----QY------OCQRRCQEQQRQHG 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                DPQRR-YQDCRQHCQQEERRLRPHCEQSCREQYEKQQQQQPDKQFKECQQRCQWQEQRPE 137
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31.4%;
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Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120; DB 2;
Pred. No. 3.6e-05;
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                                                                                                                                                of vicilin genes
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A; Residues: 1-452 <MC2>
A; Cross-references: EMBL:x62626
C; Genetics: 211/1; 269/3; 296/3; 391/3; 502/1
A; Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C; Superfamily: 9lycinin
C; Keywords: seed; storage protein
F; 1-24/Domain: signal sequence #status predicted.
F; 25-566/Product: vicilin #status predicted.
                                                                                 R:Yamada, K.: Shimada, T.; Kondo, M.; Nishimura, M. J. Biol. Chem. 274, 2563-2570, 1999
A:Title: Multiple functional proteins are produced A:Reference number: Z22767; MUID:99107919
                                                                                                                                                      protein PV100 [imported] - winter squash C;Species: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-J. C;Accession: T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
C;Superfamily: glycinin
C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;174-190/Product: globulin Beg1 #status predicted
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062
                   A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-810 <YAM>
                                                                   A; Accession: T44430
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A; Residues: 1-637 <HEC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision
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                                                                                                                                      T.; Kondo, M.; Nishimura, M.; Hara-Nishimura,
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Pred. No.
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                                                     from GB/EMBL/DDBJ
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A;Cross-references: G
A;Experimental source
C;Genetics:
A;Gene: VCA0171
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                  C;Accession: D82493
R;Heldelberg, J.E; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Newfeld, S.J.; Tachida, H.; Yedvobnick, B. J. Mol. Evol. 38, 637-641, 1994
A; Title: Drive-selection equilibrium: homopolymer A; Reference number: Z17850; MUID:94365848
A; Accession: T13998
                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein VCA0171 [imported] - Vibrio cholerae (group O1 C;Species: Vibrio cholerae (group O1 C;Species: Vibrio cholerae (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
D82493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene mastermind protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C:Accession: T13998
C:Accession: T13998
R:Newfeld, S.J.: Tachida, H.: Yedvobnick, B.
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                                                            Qy
                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-646 <HEI>
                                                                                                                                                                                                                                                                                                      A;Title: DNA Sequence of both chromosomes of A;Reference number: A82035; MUID:20406833 A;Accession: D82493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated A;Molecule type: DNA
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Matches 20
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61
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                              KRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEE 60
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source: serogroup
                                                                                              Conservative
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                                                                                                                                                                                                                       GB:AE003853; NID:g9657547; Ol; strain N16961; biotype
                                                                                                           Score 81;
Pred. No.
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Pred.
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No. 0.23;
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C;Function: modulates cell response to change A; Description: modulates cell response to change C; Superfamily: response regulator homology C; Keywords: phosphoprotein; signal transduction F; 1520-1629/Domain: response regulator homology F; 1568/Binding site: phosphate (Asp) (covalent)
A; Map position: 1
C; Superfamily: unassigned DEAD/H box helicases;
                                                                                    C; Genetics:
                                                                                                          A:Cross-references: EMBL:AF000197; NID:q1947004; PID:q1947009; PIDN:AAB52901.1; GSPDB A;Experimental source: strain Bristol N2; clone T21G5
                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-604 <MIN>
                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                    A; Reference number: Z18299
A; Accession: T15132
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosm
                                                                                                                                                                                                                                                                                                                                                                ATP-dependent RNA helicase GLH-1 - Caenorhabditis elegans (fragment) C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 26-MC;Accession: T15132
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Best Local Similarity
Thes 22; Conserv
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A; Residues: 1-149, 'E', 151-219, 'TRVLKLIQSTNNWIYWY', 238-1671 <SCW>
A; Cross-references: EMBL: X96869; NID: 91237201; PIDN: CAA65612.1;
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A; Accession: $78068
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R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
submitted to the EMBL Data Library, March 1996
A;Description: The hyprid histidine kinase DokA is part of the osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: DNA
A;Residues: 1-1670 <SCH>
A;Cross-references: EMBL:X96869
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R;Schuster, S.C.; Noegel, A
EMBO J. 15, 3880-3889, 1996
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C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: dokA
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                                                       CESP:glh-1
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                                                                                                                                                                                                            from GB/EMBL/DDBC
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  DEAD/H box helicase homology
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C;Keywords: cornified cell envelope;
F;153-386/Region: 10-residue repeats
                                                                                                 A;Introns: #status absent C;Superfamily: involucrin
                                                                                                                                                         A;Cross-references: GB:M67478; NID:g176629; PIDN:AAA35405.1; PID C;Comment: During the terminal differentiation of keratinocytes, linked envelope under the plasma membrane.
                                                                                                                                                                                                                                              A;Reference number: A57783; MUID:92114750
A;Accession: I36930
A:Moleonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 90, 9300-9304, 1993
A;Title: glh-1, a germ-line putative RNA helicase from Caenorhabditis,
A:Reference number: A48686; MUID:94022363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
A48686
                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                R; Phillips, M.A.; Rice, R.H.; Djian, P.; Green, Mol. Biol. Evol. 8, 579-591, 1991
                                                                                                                                                                                                                                                                                                                                                                      involucrin - white-fronted capuchin
C;Species: Cebus albifrons (white-fronted capuchin, pale-fronted capuchin)
C;Date: 16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-707 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable RNA helicase glh-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Jun-1998
C;Accession: A48686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Roussell, D.L.; Bennett, K.L.
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     Query Match
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Matches 22; Conserv
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Best Local
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       59
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Pred. No.
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Pred. No. 0.84;
     Score
                                                           duplication; epidermis; tandem repeat
(Q-E-G-Q-[PLV]-[KE]-[LH]-[PL]-E-Q)
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     77;
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     Length 428;
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tes, this protein
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Query Match
Best Local Similarity
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A;Status, France, A;Status, Process type: DNA A;Molecule type: DNA A;Molecules: 1-411 <BRA> A;Residues: 1-411 <BRA> A;Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1.6
C:Superfamily: involucrin
C:Keywords: cornified cell envelope;
F:152-451/Region: 10-residue repeats
                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-493 <RES>
A;Cross-references: GB:M67477; NID:g343313; PIDN:AAA36950.1; PID:g343314
C;Comment: During the terminal differentiation of keratinocytes, this protein from
                                                                                                                                                                                                                                                                                                                 involucrin - cotton-top tamarin

(;Speciles: Saguinus oedipus (cotton-top tamarin)

C;Date: 16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 22-Jun-1999

C;Accession: A57783

R;Phillips, M.A.; Rice, R.H.; Djian, P.; Green, H.

Mol. Biol. Evol. 8, 579-591, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:ACCESSAUM, H.; Wohldmann, P.
R:Bradshaw, H.; Wohldmann, P.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                 A; Title: The involucrin genes of the white-fronted A; Reference number: A57783; MUID:92114750 A; Accession: A57783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T01D1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                              A; Introns: #status absent
                                                                                                       C; Genetics:
                                                                                                                             linked envelope under the plasma membrane
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A; Introns: 25/3; 304/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 HLEQEEKQLEHP 325
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7; Mismatches
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Pred. No. 0.97;
  duplication; epidermis; tandem repeat
(Q-E-G-Q-[PLV]-[KE]-[LH]-{PL}-E-Q)
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Score Pred.

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Length 493;

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trophoblast-endothelial-activated lymphocyte surface protein 721P - human % (Reference names: gene XE7 protein C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C:Accession: A46419; I68598 R:Voland, J.R.: Myzykowski, R.J.; Huang, M.; Dutton, R.W. R:Voland, J.R.: Myzykowski, R.J.; Huang, M.; Dutton, R.W. Proc. Natl. Acad. Sci. U.S.A. 89, 10425-10429, 1992 A:Title: Cloning and sequencing of a trophoblast-endothelial-activated lymphocyte surface A:Reference number: A46419; MUID:93066251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-384,'L' <RES>
A;Cross-references: GB:L03426; NID:g340386; PIDN:AAA61303.1; PID:g340387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone (NCBIN:117872, NCBIP:117873)
R; Ellison, J.W.; Ramos, C.; Yen, P.H.; Shapiro, L.J.
Hum. Mol. Genet. 1, 691-696, 1992
A; Title: Structure and expression of the human pseudoautosomal gene XE7.
A; Reference number: 154325; MUID:93258310
A; Accession: 168598
A; Status: preliminary; translated from GB/EMBL/DDBJ
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Search completed: March
Job time: 563 sec
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A; Introns: 254/3; 304/2; 384/3
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                           470 PADRVVRLCERHHAAPPRGPAPGRCPQGEPG-PPRGRRRSQKRERERGRGG----PMQGG 524
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                                                                                                                   525 S 525
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